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- (i) expressing in the storage organ of the plant a chimeric gene comprising a nucleotide sequence encoding a sulphur-rich protein placed operably in connection with a promoter sequence capable of conferring expression in said storage organ; and
 - (ii) determining the content or composition, or content and composition, of a metabolite in the storage organ, said metabolite selected from the group consisting of oil (fatty acid), starch, soluble non-starch polysaccharide, insoluble non-starch polysaccharide, fibre and protein nitrogen, subject to the proviso that the modified metabolites do not consist of only the sulfurous protein content of a seed and/or wherein the content of an amino acid is modified, such modification is not the result of the presence of a naturally or artificially high level of that amino acid in the sulfur-rich protein.
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- 4. (Twice Amended) The method according to claim 1 wherein the metabolite is selected from the group consisting of the total protein nitrogen content of seeds, the fatty acid content of seeds, the fatty acid composition of seeds, the fibre content of seeds and the fibre quality of seeds.
 - 5. (Once Amended) The method according to claim 1 wherein the total protein nitrogen content is increased.
 - 6. (Once Amended) The method according to claim 1 wherein the fibre content or composition is modified.
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- 8. (Once Amended) The method according to claim 1 wherein the fatty acid content is increased or decreased.
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B4 11. (Twice Amended) The method according to claim 1 wherein the sulfur-rich protein comprises an amino acid sequence that is rich in methionine and/or cysteine.

B5 14. (Twice Amended) The method according to claim 1 wherein the plant is a dicotyledonous plant.

B6 16. (Twice Amended) The method according to claim 1 wherein the promoter sequence comprises the pea vicilin gene promoter sequence.

17. (Twice Amended) The method according to claim 1 wherein the plant is a monocotyledonous plant.

B7 19. (Twice Amended) The method according to claim 1 wherein the promoter comprises a *Triticum aestivum* HMW glutenin promoter sequence.

20. (Twice amended) The method according to claim 1 further comprising the first steps of:

(i) introducing the chimeric gene into a plant cell, tissue, organ or whole organism; and

(ii) regenerating an intact plant therefrom.

SB C2 21. (Once Amended) A method of increasing the protein nitrogen content of seeds of a plant, said method comprising:

(i) expressing in the seeds of the plant a chimeric gene comprising a nucleotide sequence encoding a sulphur-rich protein placed operably in connection with

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a promoter sequence capable of conferring expression in said seeds, said nucleotide sequence also positioned upstream of a transcription termination sequence; and

- (ii) determining the level of protein nitrogen in the seeds, subject to the proviso that the sulfurous protein content of the seed alone is not increased.

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24. (Twice Amended) The method according to claim 22 wherein the plant is pea or chickpea.

27. (Twice Amended) The method according to claim 25 wherein the plant is a rice plant.

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28. (Once Amended) A method of modifying the fatty acid content of seeds of a plant, said method comprising (i) expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding SSA placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant; and (ii) determining the level of a fatty acid in the seeds.

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33. (Once Amended) A method of modifying the fatty acid composition of seeds of a plant, said method comprising (i) expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding SSA placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant; and (ii) determining the level of a fatty acid in the seeds.

37. (Twice Amended) The method according to claim 33 wherein the fatty acid is selected from the group consisting of: myristic acid, stearic acid, gadoleic acid, behenic acid, lignoceric acid, oleic acid, linoleic acid, linolenic acid and erucic acid.

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Sub C⁴ 38. (Once Amended) A method of decreasing the starch content of seeds of a plant, said method comprising (i) expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding SSA placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant; and (ii) determining the starch content of the seeds.

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Sub C⁵ 42. (Once Amended) A method of modifying the amino acid composition of seeds of a plant, said method comprising (i) of expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding SSA placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant; and (ii) determining the amino acid composition of the seeds, subject to the proviso that said modified composition is not the result of the presence of a naturally or artificially high level of that amino acid in a sulfur-rich protein.

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Sub C⁶ 47. (Once Amended) A method of modifying the fibre content of seeds of a plant, said method comprising (i) expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding SSA placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant; and (ii) determining the fibre content of the seeds.

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52. (Once Amended) A method of modifying the fibre quality of seeds of a plant, said method (i) comprising the step of expressing in the seeds of said plant a chimeric gene that comprises a structural gene sequence encoding SSA placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant; and (ii) determining the fibre quality of the seeds.

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64. (Twice Amended) The method according to any one of claims 21, 28, 33, 38, 42, 47 or 52, further comprising the first steps of:

(i) introducing the chimeric gene into a plant cell, tissue, organ or whole organism; and

(ii) regenerating an intact plant therefrom.

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65. (Twice Amended) A transformed plant produced by the method according to any one of claims 1, 21, 28, 33, 38, 42, 47, or 52 or progeny of said plant, wherein said progeny comprises at least one copy of the chimeric gene in an expressible format.

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67. (Twice Amended) A plant part derived from the plant according to claim 65 wherein said plant part comprises at least one copy of the chimeric gene present in said plant or progeny in an expressible format.

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68. (Once Amended) The plant part according to claim 67 selected from the group consisting of: leaves, stems, roots, shoots, seed, tubers and flowers.

69. (Once Amended) The plant part according to claim 67 consisting of seeds.

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86. (Once Amended) The method according to claim 1 wherein the storage organ is a tuber.

87. (Once Amended) The method according to claim 1 wherein the storage organ is a specialised stem.

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88. (Once Amended) The method of claim 1 wherein the chimeric gene encodes sunflower seed albumin (SSA) and wherein the storage organ is a seed and wherein the total protein nitrogen content of the seed is increased.

89. (Once Amended) The method of claim 1 wherein the chimeric gene encodes sunflower seed albumin (SSA) and wherein the storage organ is a seed and wherein the amino acid composition of the seed is modified.

90. (Once Amended) The method of claim 1 wherein the chimeric gene encodes sunflower seed albumin (SSA) and wherein the storage organ is a seed and wherein expression of the chimeric gene in the seed increases or decreases the fibre content of the seed.

91. (Once Amended) The method of claim 1 wherein the chimeric gene encodes sunflower seed albumin (SSA) and wherein the storage organ is a seed and wherein expression of the chimeric gene in the seed modifies the fibre composition of the seed.

92. (Once Amended) The method of claim 1 wherein the chimeric gene encodes sunflower seed albumin (SSA) and wherein the storage organ is a seed and wherein

expression of the chimeric gene in the seed decreases the total starch content of the seed.

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93. (Once Amended) The method of claim 1 wherein the chimeric gene encodes sunflower seed albumin (SSA) and wherein the storage organ is a seed and wherein expression of the chimeric gene in the seed increases or decreases the total fatty acid content of the seed.

94. (Once Amended) The method of claim 1 wherein the chimeric gene encodes sunflower seed albumin (SSA) and wherein the storage organ is a seed and wherein expression of the chimeric gene in the seed modifies the fatty acid composition of the seed.

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96. (Once Amended) The method of claim 1 wherein the chimeric gene encodes sunflower seed albumin (SSA) and further comprises a promoter sequence which confers strong expression at least in the seeds of the plant.

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99. (Once Amended) The method of claim 96 wherein the chimeric gene further comprises a transcription terminator sequence placed downstream of the sequence encoding SSA.

100. (Once Amended) The method of claim 99 wherein the transcription terminator sequence is the pea vicilin gene terminator sequence.
